

SEQUENCE LISTING

<110> CHATFIELD, STEVEN N.

<120> ATTENUATED BACTERIA USEFUL IN VACCINES

<130> 117-320

<140> US 09/646,925

<141>

<150> PCT/GB99/00935

<151> 1999-03-25

<150> GB 9806449.6

<151> 1998-03-25

<160> 28

<170> PatentIn Ver. 2.1

<210> 1

<211> 1690

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (492)..(1562)

<400> 1

```

gtcgcgcgcg tggatatctc tccagacgcg ctggcgggtg ctgaacagaa catcgaagaa 60
cacggtctga tccacaacgt cattccgatt cgttccgata tgttccgcga cttgccgaaa 120
gtgcagtacg acctgattgt cactaaccgc ccgtatgtcg atgcgaagat atgtccgacc 180
tgccaaacaa taccgccacg agccggaact gggcctggca tctggcactg acggcctgaa 240
actgacgcgt cgcattctcg gtaacgcggc agattacctt gctgatgatg gcgtgttgat 300
ttgtgaagtc ggcaacagca tggtagatct tatggaacaa tatccggatg ttccgttcac 360
ctggctggag tttgataacg gcggcgatgg tgtgtttatg ctcaccaaag agcagcttat 420
tgccgcacga gaacatttcg cgatttataa agattaagta aacacgcaaa cacaacaata 480
acggagccgt g atg gct gga aac aca att gga caa ctc ttt cgc gta acc 530
          Met Ala Gly Asn Thr Ile Gly Gln Leu Phe Arg Val Thr
              1              5              10

acc ttc ggc gaa tcg cac ggg ctg gcg ctc ggc tgc atc gtc gat ggt 578
Thr Phe Gly Glu Ser His Gly Leu Ala Leu Gly Cys Ile Val Asp Gly
      15              20              25

gtt ccg cca ggc att ccg ctg acg gaa gcg gac ctg caa cat gac ctc 626
Val Pro Pro Gly Ile Pro Leu Thr Glu Ala Asp Leu Gln His Asp Leu

```

30	35	40	45	
gac cgt cgt cgc cct ggg aca tcg cgc tat acc acc cag cgc cgc gag				674
Asp Arg Arg Arg Pro Gly Thr Ser Arg Tyr Thr Thr Gln Arg Arg Glu				
	50	55	60	
ccg gat cag gtc aaa att ctc tcc ggt gtt ttt gaa ggc gtt act acc				722
Pro Asp Gln Val Lys Ile Leu Ser Gly Val Phe Glu Gly Val Thr Thr				
	65	70	75	
ggc acc agc att ggc ttg ttg atc gaa aac act gac cag cgc tct cag				770
Gly Thr Ser Ile Gly Leu Leu Ile Glu Asn Thr Asp Gln Arg Ser Gln				
	80	85	90	
gat tac agt gcg att aag gac gtt ttc cgt cca ggc cat gcc gat tac				818
Asp Tyr Ser Ala Ile Lys Asp Val Phe Arg Pro Gly His Ala Asp Tyr				
	95	100	105	
acc tac gaa caa aaa tac ggt ctg cgc gat tat cgc ggc ggt gga cgt				866
Thr Tyr Glu Gln Lys Tyr Gly Leu Arg Asp Tyr Arg Gly Gly Gly Arg				
	110	115	120	125
tct tcc gcc cgc gaa acc gcc atg cgc gtg gcg gca gga gct att gcc				914
Ser Ser Ala Arg Glu Thr Ala Met Arg Val Ala Ala Gly Ala Ile Ala				
	130	135	140	
aaa aaa tat ctc gcc gag aaa ttt ggt att gaa atc cgt ggc tgc ctg				962
Lys Lys Tyr Leu Ala Glu Lys Phe Gly Ile Glu Ile Arg Gly Cys Leu				
	145	150	155	
acc cag atg ggc gac att ccg ctg gat atc aaa gac tgg tcg cag gtc				1010
Thr Gln Met Gly Asp Ile Pro Leu Asp Ile Lys Asp Trp Ser Gln Val				
	160	165	170	
gag caa aat ccg ttt ttt tgc ccg gac ccc gac aaa atc gac gcg tta				1058
Glu Gln Asn Pro Phe Phe Cys Pro Asp Pro Asp Lys Ile Asp Ala Leu				
	175	180	185	
gac gag ttg atg cgt gcg ctg aaa aaa gag ggc gac tcc atc ggc gct				1106
Asp Glu Leu Met Arg Ala Leu Lys Lys Glu Gly Asp Ser Ile Gly Ala				
	190	195	200	205
aaa gtc acc gtt gtt gcc agt ggc gtt cct gcc gga ctt ggc gag ccg				1154
Lys Val Thr Val Val Ala Ser Gly Val Pro Ala Gly Leu Gly Glu Pro				
	210	215	220	
gtc ttt gac cgc ctg gat gct gac atc gcc cat gcg ctg atg agc atc				1202
Val Phe Asp Arg Leu Asp Ala Asp Ile Ala His Ala Leu Met Ser Ile				
	225	230	235	
aac gcg gtg aaa ggc gtg gaa att ggc gac ggc ttt gac gtg gtg gcg				1250
Asn Ala Val Lys Gly Val Glu Ile Gly Asp Gly Phe Asp Val Val Ala				
	240	245	250	
ctg cgc ggc agc cag aac cgc gat gaa atc acc aaa gac ggt ttc cag				1298
Leu Arg Gly Ser Gln Asn Arg Asp Glu Ile Thr Lys Asp Gly Phe Gln				
	255	260	265	

agc aac cat gcg ggc ggc att ctc ggc ggt atc agc agc ggg cag caa 1346
 Ser Asn His Ala Gly Gly Ile Leu Gly Gly Ile Ser Ser Gly Gln Gln
 270 275 280 285
 atc att gcc cat atg gcg ctg aaa ccg acc tcc agc att acc gtg ccg 1394
 Ile Ile Ala His Met Ala Leu Lys Pro Thr Ser Ser Ile Thr Val Pro
 290 295 300
 ggt cgt acc att aac cgc ttt ggc gaa gaa gtt gag atg atc acc aaa 1442
 Gly Arg Thr Ile Asn Arg Phe Gly Glu Glu Val Glu Met Ile Thr Lys
 305 310 315
 ggc cgt cac gat ccc tgt gtc ggg atc cgc gca gtg ccg atc gca gaa 1490
 Gly Arg His Asp Pro Cys Val Gly Ile Arg Ala Val Pro Ile Ala Glu
 320 325 330
 gcg aat gct ggc gat cgt ttt aat gga tca cct gtt acg gca acg ggc 1538
 Ala Asn Ala Gly Asp Arg Phe Asn Gly Ser Pro Val Thr Ala Thr Gly
 335 340 345
 gca aaa tgc cga tgt gaa gac tga tattccacgc tggtaaaaaa tgaataaaac 1592
 Ala Lys Cys Arg Cys Glu Asp
 350 355
 cgcgattgcg ctgctggctc tgcttgccag tagcgccagc ctggcagcga cgccgtggca 1652
 aaaaataacc caacctgtgc cgggtagcgc caaatcga 1690

<210> 2
 <211> 356
 <212> PRT
 <213> Escherichia coli

<400> 2
 Met Ala Gly Asn Thr Ile Gly Gln Leu Phe Arg Val Thr Thr Phe Gly
 1 5 10 15
 Glu Ser His Gly Leu Ala Leu Gly Cys Ile Val Asp Gly Val Pro Pro
 20 25 30
 Gly Ile Pro Leu Thr Glu Ala Asp Leu Gln His Asp Leu Asp Arg Arg
 35 40 45
 Arg Pro Gly Thr Ser Arg Tyr Thr Thr Gln Arg Arg Glu Pro Asp Gln
 50 55 60
 Val Lys Ile Leu Ser Gly Val Phe Glu Gly Val Thr Thr Gly Thr Ser
 65 70 75 80
 Ile Gly Leu Leu Ile Glu Asn Thr Asp Gln Arg Ser Gln Asp Tyr Ser
 85 90 95
 Ala Ile Lys Asp Val Phe Arg Pro Gly His Ala Asp Tyr Thr Tyr Glu
 100 105 110

Gln Lys Tyr Gly Leu Arg Asp Tyr Arg Gly Gly Gly Arg Ser Ser Ala
 115 120 125
 Arg Glu Thr Ala Met Arg Val Ala Ala Gly Ala Ile Ala Lys Lys Tyr
 130 135 140
 Leu Ala Glu Lys Phe Gly Ile Glu Ile Arg Gly Cys Leu Thr Gln Met
 145 150 155 160
 Gly Asp Ile Pro Leu Asp Ile Lys Asp Trp Ser Gln Val Glu Gln Asn
 165 170 175
 Pro Phe Phe Cys Pro Asp Pro Asp Lys Ile Asp Ala Leu Asp Glu Leu
 180 185 190
 Met Arg Ala Leu Lys Lys Glu Gly Asp Ser Ile Gly Ala Lys Val Thr
 195 200 205
 Val Val Ala Ser Gly Val Pro Ala Gly Leu Gly Glu Pro Val Phe Asp
 210 215 220
 Arg Leu Asp Ala Asp Ile Ala His Ala Leu Met Ser Ile Asn Ala Val
 225 230 235 240
 Lys Gly Val Glu Ile Gly Asp Gly Phe Asp Val Val Ala Leu Arg Gly
 245 250 255
 Ser Gln Asn Arg Asp Glu Ile Thr Lys Asp Gly Phe Gln Ser Asn His
 260 265 270
 Ala Gly Gly Ile Leu Gly Gly Ile Ser Ser Gly Gln Gln Ile Ile Ala
 275 280 285
 His Met Ala Leu Lys Pro Thr Ser Ser Ile Thr Val Pro Gly Arg Thr
 290 295 300
 Ile Asn Arg Phe Gly Glu Glu Val Glu Met Ile Thr Lys Gly Arg His
 305 310 315 320
 Asp Pro Cys Val Gly Ile Arg Ala Val Pro Ile Ala Glu Ala Asn Ala
 325 330 335
 Gly Asp Arg Phe Asn Gly Ser Pro Val Thr Ala Thr Gly Ala Lys Cys
 340 345 350
 Arg Cys Glu Asp
 355

<210> 3
 <211> 1713
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (491)..(1594)

<400> 3

```
gttaacaagc gttatagttt ttctgtggta gcacagaata atgaaaagtg tgtaaagaag 60
ggtaaaaaaa accgaatgcg aggcattccgg ttgaaatagg ggtaaacaga cattcagaaa 120
tgaatgacgg taataaataa agttaatgat gatagcggga gttattctag ttgcgagtga 180
aggttttggt ttgacattca gtgctgtcaa atacttaaga ataagttatt gattttaacc 240
ttgaattatt attgcttgat gttagggtgct tatttcgcca ttccgcaata atcttaaaaa 300
gttcccttgc atttacattt tgaacatct atagcgataa atgaaacatc ttaaaagttt 360
tagtatcata ttcgtgttgg attattctgc atttttgggg agaatggact tgccgactga 420
ttaatgaggg ttaatcagta tgcagtggca taaaaaagca aataaaggca tataacagag 480
ggtaataaac atg aaa gtt aaa gta ctg tcc ctc ctg gtc cca gct ctg 529
          Met Lys Val Lys Val Leu Ser Leu Leu Val Pro Ala Leu
            1             5             10
ctg gta gca ggc gca gca aac gct gct gaa gtt tac aac aaa gac ggc 577
Leu Val Ala Gly Ala Ala Asn Ala Ala Glu Val Tyr Asn Lys Asp Gly
      15             20             25
aac aaa tta gat ctg tac ggt aaa gta gac ggc ctg cac tat ttc tct 625
Asn Lys Leu Asp Leu Tyr Gly Lys Val Asp Gly Leu His Tyr Phe Ser
      30             35             40             45
gac aac aaa gat gta gat ggc gac cag acc tac atg cgt ctt ggc ttc 673
Asp Asn Lys Asp Val Asp Gly Asp Gln Thr Tyr Met Arg Leu Gly Phe
            50             55             60
aaa ggt gaa act cag gtt act gac cag ctg acc ggt tac ggc cag tgg 721
Lys Gly Glu Thr Gln Val Thr Asp Gln Leu Thr Gly Tyr Gly Gln Trp
            65             70             75
gaa tat cag atc cag ggc aac agc gct gaa aac gaa aac aac tcc tgg 769
Glu Tyr Gln Ile Gln Gly Asn Ser Ala Glu Asn Glu Asn Asn Ser Trp
            80             85             90
acc cgt gtg gca ttc gca ggt ctg aaa ttc cag gat gtg ggt tct ttc 817
Thr Arg Val Ala Phe Ala Gly Leu Lys Phe Gln Asp Val Gly Ser Phe
            95             100             105
gac tac ggt cgt aac tac ggc gtt gtt tat gac gta act tcc tgg acc 865
Asp Tyr Gly Arg Asn Tyr Gly Val Val Tyr Asp Val Thr Ser Trp Thr
      110             115             120             125
gac gta ctg cca gaa ttc ggt ggt gac acc tac ggt tct gac aac ttc 913
Asp Val Leu Pro Glu Phe Gly Gly Asp Thr Tyr Gly Ser Asp Asn Phe
            130             135             140
atg cag cag cgt ggt aac ggc ttc gcg acc tac cgt aac act gac ttc 961
Met Gln Gln Arg Gly Asn Gly Phe Ala Thr Tyr Arg Asn Thr Asp Phe
            145             150             155
```

ttc ggt ctg gtt gac ggc ctg aac ttt gct gtt cag tac cag ggt aaa	1009
Phe Gly Leu Val Asp Gly Leu Asn Phe Ala Val Gln Tyr Gln Gly Lys	
160 165 170	
aac ggc aac cca tct ggt gaa ggc ttt act agt ggc gta act aac aac	1057
Asn Gly Asn Pro Ser Gly Glu Gly Phe Thr Ser Gly Val Thr Asn Asn	
175 180 185	
ggt cgt gac gca ctg cgt caa aac ggc gac ggc gtc ggc ggt tct atc	1105
Gly Arg Asp Ala Leu Arg Gln Asn Gly Asp Gly Val Gly Gly Ser Ile	
190 195 200 205	
act tat gat tac gaa ggt ttc ggt atc ggt ggt gcg atc tcc agc tcc	1153
Thr Tyr Asp Tyr Glu Gly Phe Gly Ile Gly Gly Ala Ile Ser Ser Ser	
210 215 220	
aaa cgt act gat gct cag aac acc gct gct tac atc ggt aac ggc gac	1201
Lys Arg Thr Asp Ala Gln Asn Thr Ala Ala Tyr Ile Gly Asn Gly Asp	
225 230 235	
cgt gct gaa acc tac act ggt ggt ctg aaa tac gac gct aac aac atc	1249
Arg Ala Glu Thr Tyr Thr Gly Gly Leu Lys Tyr Asp Ala Asn Asn Ile	
240 245 250	
tac ctg gct gct cag tac acc cag acc tac aac gca act cgc gta ggt	1297
Tyr Leu Ala Ala Gln Tyr Thr Gln Thr Tyr Asn Ala Thr Arg Val Gly	
255 260 265	
tcc ctg ggt tgg gcg aac aaa gca cag aac ttc gaa gct gtt gct cag	1345
Ser Leu Gly Trp Ala Asn Lys Ala Gln Asn Phe Glu Ala Val Ala Gln	
270 275 280 285	
tac cag ttc gac ttc ggt ctg cgt ccg tcc ctg gct tac ctg cag tct	1393
Tyr Gln Phe Asp Phe Gly Leu Arg Pro Ser Leu Ala Tyr Leu Gln Ser	
290 295 300	
aaa ggt aaa aac ctg ggt cgt ggc tac gac gac gaa gat atc ctg aaa	1441
Lys Gly Lys Asn Leu Gly Arg Gly Tyr Asp Asp Glu Asp Ile Leu Lys	
305 310 315	
tat gtt gat gtt ggt gct acc tac tac ttc aac aaa aac atg tcc acc	1489
Tyr Val Asp Val Gly Ala Thr Tyr Tyr Phe Asn Lys Asn Met Ser Thr	
320 325 330	
tac gtt gac tac aaa atc aac ctg ctg gac gac aac cag ttc act cgt	1537
Tyr Val Asp Tyr Lys Ile Asn Leu Leu Asp Asp Asn Gln Phe Thr Arg	
335 340 345	
gac gct ggc atc aac act gat aac atc gta gct ctg ggt ctg gtt tac	1585
Asp Ala Gly Ile Asn Thr Asp Asn Ile Val Ala Leu Gly Leu Val Tyr	
350 355 360 365	
cag ttc taa tctcgattga tatcgaacaa gggcctgcgg gccctttttt	1634
Gln Phe	
cattgttttc agcgtacaaa ctacgttttt tgggtgtactc ttgcgaccgt tcgcatgagg	1694

ataatcacgt acggaaata

1713

<210> 4

<211> 367

<212> PRT

<213> Escherichia coli

<400> 4

Met Lys Val Lys Val Leu Ser Leu Leu Val Pro Ala Leu Leu Val Ala
1 5 10 15

Gly Ala Ala Asn Ala Ala Glu Val Tyr Asn Lys Asp Gly Asn Lys Leu
20 25 30

Asp Leu Tyr Gly Lys Val Asp Gly Leu His Tyr Phe Ser Asp Asn Lys
35 40 45

Asp Val Asp Gly Asp Gln Thr Tyr Met Arg Leu Gly Phe Lys Gly Glu
50 55 60

Thr Gln Val Thr Asp Gln Leu Thr Gly Tyr Gly Gln Trp Glu Tyr Gln
65 70 75 80

Ile Gln Gly Asn Ser Ala Glu Asn Glu Asn Asn Ser Trp Thr Arg Val
85 90 95

Ala Phe Ala Gly Leu Lys Phe Gln Asp Val Gly Ser Phe Asp Tyr Gly
100 105 110

Arg Asn Tyr Gly Val Val Tyr Asp Val Thr Ser Trp Thr Asp Val Leu
115 120 125

Pro Glu Phe Gly Gly Asp Thr Tyr Gly Ser Asp Asn Phe Met Gln Gln
130 135 140

Arg Gly Asn Gly Phe Ala Thr Tyr Arg Asn Thr Asp Phe Phe Gly Leu
145 150 155 160

Val Asp Gly Leu Asn Phe Ala Val Gln Tyr Gln Gly Lys Asn Gly Asn
165 170 175

Pro Ser Gly Glu Gly Phe Thr Ser Gly Val Thr Asn Asn Gly Arg Asp
180 185 190

Ala Leu Arg Gln Asn Gly Asp Gly Val Gly Gly Ser Ile Thr Tyr Asp
195 200 205

Tyr Glu Gly Phe Gly Ile Gly Gly Ala Ile Ser Ser Ser Lys Arg Thr
210 215 220

Asp Ala Gln Asn Thr Ala Ala Tyr Ile Gly Asn Gly Asp Arg Ala Glu
225 230 235 240

Thr Tyr Thr Gly Gly Leu Lys Tyr Asp Ala Asn Asn Ile Tyr Leu Ala
245 250 255

Ala Gln Tyr Thr Gln Thr Tyr Asn Ala Thr Arg Val Gly Ser Leu Gly
260 265 270

Trp Ala Asn Lys Ala Gln Asn Phe Glu Ala Val Ala Gln Tyr Gln Phe
275 280 285

Asp Phe Gly Leu Arg Pro Ser Leu Ala Tyr Leu Gln Ser Lys Gly Lys
290 295 300

Asn Leu Gly Arg Gly Tyr Asp Asp Glu Asp Ile Leu Lys Tyr Val Asp
305 310 315 320

Val Gly Ala Thr Tyr Tyr Phe Asn Lys Asn Met Ser Thr Tyr Val Asp
325 330 335

Tyr Lys Ile Asn Leu Leu Asp Asp Asn Gln Phe Thr Arg Asp Ala Gly
340 345 350

Ile Asn Thr Asp Asn Ile Val Ala Leu Gly Leu Val Tyr Gln Phe
355 360 365

<210> 5
<211> 1808
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (457)..(1545)

<400> 5
aaaactaatc cgcattctta ttgcggatta gttttttctt agctaatagc acaattttca 60
tactatTTTT tggcattctg gatgtctgaa agaagatttt gtgccaggtc gataaagttt 120
ccatcagaaa caaaatttcc gtttagtta tttaaatata aggaaatcat ataaatagat 180
taaaattgct gtaaatatca tcacgtctct atggaaatat gacggtgttc acaaagttcc 240
ttaaatttta cttttggta catatTTTT ctttttgaaa ccaaattttt atctttgtag 300
cactttcacg gtagcgaaac gtttagtttga atggaaagat gcctgcagac acataaagac 360
accaaactct catcaatagt tccgtaaatt tttattgaca gaacttattg acggcagtg 420
caggtgtcat aaaaaaaacc atgagggtaa taaata atg atg aag cgc aat att 474
Met Met Lys Arg Asn Ile
1 5
ctg gca gtg atc gtc cct gct ctg tta gta gca ggt act gca aac gct 522
Leu Ala Val Ile Val Pro Ala Leu Leu Val Ala Gly Thr Ala Asn Ala
10 15 20
gca gaa atc tat aac aaa gat ggc aac aaa gta gat ctg tac ggt aaa 570
Ala Glu Ile Tyr Asn Lys Asp Gly Asn Lys Val Asp Leu Tyr Gly Lys
25 30 35

gct gtt ggt ctg cat tat ttt tcc aag ggt aac ggt gaa aac agt tac	618
Ala Val Gly Leu His Tyr Phe Ser Lys Gly Asn Gly Glu Asn Ser Tyr	
40 45 50	
ggt ggc aat ggc gac atg acc tat gcc cgt ctt ggt ttt aaa ggg gaa	666
Gly Gly Asn Gly Asp Met Thr Tyr Ala Arg Leu Gly Phe Lys Gly Glu	
55 60 65 70	
act caa atc aat tcc gat ctg acc ggt tat ggt cag tgg gaa tat aac	714
Thr Gln Ile Asn Ser Asp Leu Thr Gly Tyr Gly Gln Trp Glu Tyr Asn	
75 80 85	
ttc cag ggt aac aac tct gaa ggc gct gac gct caa act ggt aac aaa	762
Phe Gln Gly Asn Asn Ser Glu Gly Ala Asp Ala Gln Thr Gly Asn Lys	
90 95 100	
acg cgt ctg gca ttc gcg ggt ctt aaa tac gct gac gtt ggt tct ttc	810
Thr Arg Leu Ala Phe Ala Gly Leu Lys Tyr Ala Asp Val Gly Ser Phe	
105 110 115	
gat tac ggc cgt aac tac ggt gtg gtt tat gat gca ctg ggt tac acc	858
Asp Tyr Gly Arg Asn Tyr Gly Val Val Tyr Asp Ala Leu Gly Tyr Thr	
120 125 130	
gat atg ctg cca gaa ttt ggt ggt gat act gca tac agc gat gac ttc	906
Asp Met Leu Pro Glu Phe Gly Gly Asp Thr Ala Tyr Ser Asp Asp Phe	
135 140 145 150	
ttc gtt ggt cgt gtt ggc ggc gtt gct acc tat cgt aac tcc aac ttc	954
Phe Val Gly Arg Val Gly Gly Val Ala Thr Tyr Arg Asn Ser Asn Phe	
155 160 165	
ttt ggt ctg gtt gat ggc ctg aac ttc gct gtt cag tac ctg ggt aaa	1002
Phe Gly Leu Val Asp Gly Leu Asn Phe Ala Val Gln Tyr Leu Gly Lys	
170 175 180	
aac gag cgt gac act gca cgc cgt tct aac ggc gac ggt gtt ggc ggt	1050
Asn Glu Arg Asp Thr Ala Arg Ser Asn Gly Asp Gly Val Gly Gly	
185 190 195	
tct atc agc tac gaa tac gaa ggc ttt ggt atc gtt ggt gct tat ggt	1098
Ser Ile Ser Tyr Glu Tyr Glu Gly Phe Gly Ile Val Gly Ala Tyr Gly	
200 205 210	
gca gct gac cgt acc aac ctg caa gaa gct caa cct ctt ggc aac ggt	1146
Ala Ala Asp Arg Thr Asn Leu Gln Glu Ala Gln Pro Leu Gly Asn Gly	
215 220 225 230	
aaa aaa gct gaa cag tgg gct act ggt ctg aag tac gac gcg aac aac	1194
Lys Lys Ala Glu Gln Trp Ala Thr Gly Leu Lys Tyr Asp Ala Asn Asn	
235 240 245	
atc tac ctg gca gcg aac tac ggt gaa acc cgt aac gct acg ccg atc	1242
Ile Tyr Leu Ala Ala Asn Tyr Gly Glu Thr Arg Asn Ala Thr Pro Ile	
250 255 260	

act aat aaa ttt aca aac acc agc ggc ttc gcc aac aaa acg caa gac 1290
 Thr Asn Lys Phe Thr Asn Thr Ser Gly Phe Ala Asn Lys Thr Gln Asp
 265 270 275
 gtt ctg tta gtt gcg caa tac cag ttc gat ttc ggt ctg cgt ccg tcc 1338
 Val Leu Leu Val Ala Gln Tyr Gln Phe Asp Phe Gly Leu Arg Pro Ser
 280 285 290
 atc gct tac acc aaa tct aaa gcg aaa gac gta gaa ggt atc ggt gat 1386
 Ile Ala Tyr Thr Lys Ser Lys Ala Lys Asp Val Glu Gly Ile Gly Asp
 295 300 305 310
 gtt gat ctg gtg aac tac ttt gaa gtg ggc gca acc tac tac ttc aac 1434
 Val Asp Leu Val Asn Tyr Phe Glu Val Gly Ala Thr Tyr Tyr Phe Asn
 315 320 325
 aaa aac atg tcc acc tat gtt gac tac atc atc aac cag atc gat tct 1482
 Lys Asn Met Ser Thr Tyr Val Asp Tyr Ile Ile Asn Gln Ile Asp Ser
 330 335 340
 gac aac aaa ctg ggc gta ggt tca gac gac acc gtt gct gtg ggt atc 1530
 Asp Asn Lys Leu Gly Val Gly Ser Asp Asp Thr Val Ala Val Gly Ile
 345 350 355
 gtt tac cag ttc taa tagcacacct ctttggttaa tgccgaaaaa acaggacttt 1585
 Val Tyr Gln Phe
 360
 ggtcctgttt tttttatacc ttccagagca atctcacgtc ttgcaaaaac agcctgcgtt 1645
 ttcacagta atagttggaa ttttgtaa atccccgttac cctgatagcg gacttccctt 1705
 ctgtaaccat aatggaacct cgtcatgttt gagaacatta ccgccgctcc tgccgacccg 1765
 attctggggc tggccgatct gtttcgtgcc gatgaacgtc ccg 1808

<210> 6
 <211>362
 <212> PRT
 <213> Escherichia coli

<400> 6
 Met Met Lys Arg Asn Ile Leu Ala Val Ile Val Pro Ala Leu Leu Val
 1 5 10 15
 Ala Gly Thr Ala Asn Ala Ala Glu Ile Tyr Asn Lys Asp Gly Asn Lys
 20 25 30
 Val Asp Leu Tyr Gly Lys Ala Val Gly Leu His Tyr Phe Ser Lys Gly
 35 40 45
 Asn Gly Glu Asn Ser Tyr Gly Gly Asn Gly Asp Met Thr Tyr Ala Arg
 50 55 60
 Leu Gly Phe Lys Gly Glu Thr Gln Ile Asn Ser Asp Leu Thr Gly Tyr
 65 70 75 80

Gly Gln Trp Glu Tyr Asn Phe Gln Gly Asn Asn Ser Glu Gly Ala Asp
85 90 95

Ala Gln Thr Gly Asn Lys Thr Arg Leu Ala Phe Ala Gly Leu Lys Tyr
100 105 110

Ala Asp Val Gly Ser Phe Asp Tyr Gly Arg Asn Tyr Gly Val Val Tyr
115 120 125

Asp Ala Leu Gly Tyr Thr Asp Met Leu Pro Glu Phe Gly Gly Asp Thr
130 135 140

Ala Tyr Ser Asp Asp Phe Phe Val Gly Arg Val Gly Gly Val Ala Thr
145 150 155 160

Tyr Arg Asn Ser Asn Phe Phe Gly Leu Val Asp Gly Leu Asn Phe Ala
165 170 175

Val Gln Tyr Leu Gly Lys Asn Glu Arg Asp Thr Ala Arg Arg Ser Asn
180 185 190

Gly Asp Gly Val Gly Gly Ser Ile Ser Tyr Glu Tyr Glu Gly Phe Gly
195 200 205

Ile Val Gly Ala Tyr Gly Ala Ala Asp Arg Thr Asn Leu Gln Glu Ala
210 215 220

Gln Pro Leu Gly Asn Gly Lys Lys Ala Glu Gln Trp Ala Thr Gly Leu
225 230 235 240

Lys Tyr Asp Ala Asn Asn Ile Tyr Leu Ala Ala Asn Tyr Gly Glu Thr
245 250 255

Arg Asn Ala Thr Pro Ile Thr Asn Lys Phe Thr Asn Thr Ser Gly Phe
260 265 270

Ala Asn Lys Thr Gln Asp Val Leu Leu Val Ala Gln Tyr Gln Phe Asp
275 280 285

Phe Gly Leu Arg Pro Ser Ile Ala Tyr Thr Lys Ser Lys Ala Lys Asp
290 295 300

Val Glu Gly Ile Gly Asp Val Asp Leu Val Asn Tyr Phe Glu Val Gly
305 310 315 320

Ala Thr Tyr Tyr Phe Asn Lys Asn Met Ser Thr Tyr Val Asp Tyr Ile
325 330 335

Ile Asn Gln Ile Asp Ser Asp Asn Lys Leu Gly Val Gly Ser Asp Asp
340 345 350

Thr Val Ala Val Gly Ile Val Tyr Gln Phe
355 360

<210> 7

<211> 35

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR primer

 <400> 7
 atctgtttgt tgagctcagc aatctatttg caacc 35

<210> 8
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR primer

 <400> 8
 ttttttgcca gcatgccggc agccacgcgt agtg 34

<210> 9
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR primer

 <400> 9
 ctcgaggctt agctctattt attaccctca tgg 33

<210> 10
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR primer

 <400> 10
 gagctaagcc tcgagtaata gcacacctct ttg 33

<210> 11
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR primer

 <400> 11
 ttgctggaaa gtcgacggat gttaattatt tgtg 34

<210> 12
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 12
ggccaaagcc gagtcattc accagcggcc cgacg 35

<210> 13
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 13
gctaagcctc gagtaatctc gattgatatc cg 32

<210> 14
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 14
ctcgaggctt agcgttatta accctctgtt a 31

<210> 15
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 15
ccgcgctcgc tctagagtga actgatcaac aata 34

<210> 16
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 16 34
 atgcgcgcga gagctcaacc agcgtcgac ttg

<210> 17
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR primer

<400> 17 30
 ctcgaggcat gctgaataaa accgcgattg

<210> 18
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR primer

<400> 18 31
 gcatgccctc gagggctccg ttattgttgt g

<210> 19
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR primer

<400> 19 25
 tgattccctt tggtgcgaag gcgaa

<210> 20
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR primer

<400> 20 25
 attaagatac ccaagtaata ctcaa

<210> 21
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 21
gcttttaaag gatcctagtt 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 22
ggttatcttt ccggattgtc 20

<210> 23
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 23
catgttccgg aggtaatatg aa 22

<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 24
agttcccttt atattattaa ta 22

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 25
tgagtttat atgaaactaa 20

<210> 26
<211> 20
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 26

tgacttagtc aggataattg

20

<210> 27

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 27

atacttatta ataggtcttt

20

<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 28

ttgtcgaagt aattgttata

20